



# assertHE: HTA R model review

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**DSMC Meeting | Robert Smith & Wael Mohammed | May 2024**

✉️ [rsmith@darkpeakanalytics.com](mailto:rsmith@darkpeakanalytics.com)

💻 <https://github.com/dark-peak-analytics>

linkedin <https://www.linkedin.com/company/dark-peak-analytics>



# Background

# Who we are



Dr. Paul Schneider



Dr. Sarah Bates



Dr. Robert Smith



Dr. Jesus Perez



Wael Mohammed



ShangShang Gu



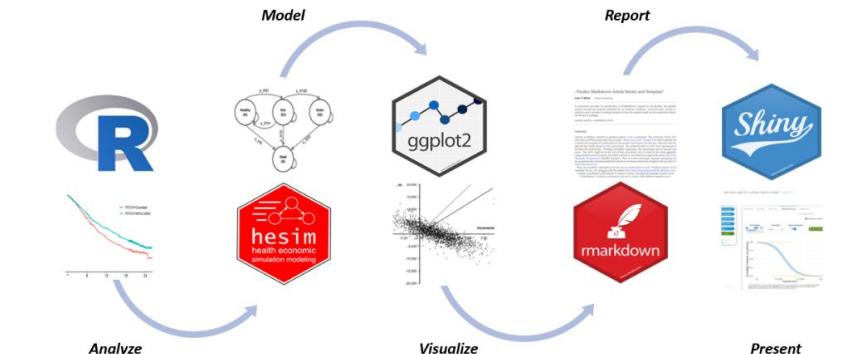
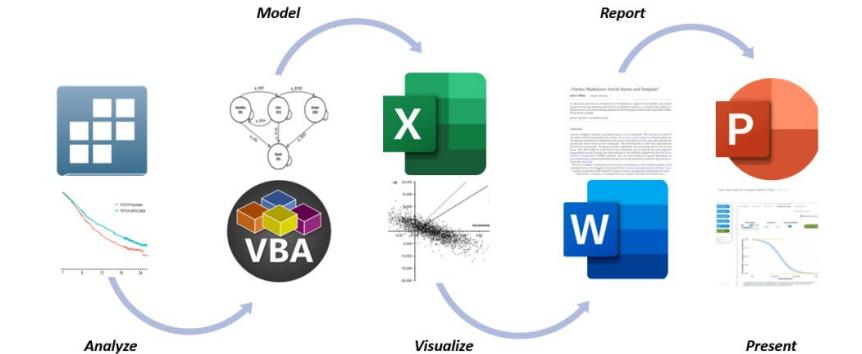
Dr. Joe Molloy



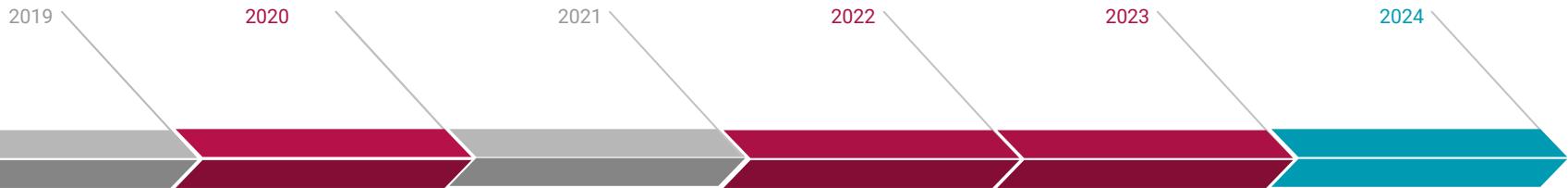
Calum Lewis

# Overarching aim

*Shifting the HTA modelling pipeline from spreadsheet software (e.g. MS Excel) to script based programming languages (e.g R).*

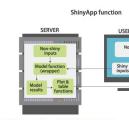


# Related publications



## Making Health Economic Models Shiny: A tutorial

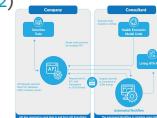
**Smith RA and Schneider PP.** Making health economic models Shiny: A tutorial. *Wellcome Open Res* 2020, **5**:69 (<https://doi.org/10.12688/wellcomeopenres.15807.2>)



covid-19 work

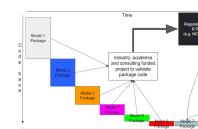
## Living HTA: Automating Health Economic Evaluation with R

**Smith RA, Schneider PP and Mohammed W.** Living HTA: Automating Health Economic Evaluation with R. *Wellcome Open Res* 2022, **7**:194 (<https://doi.org/10.12688/wellcomeopenres.17933.2>)



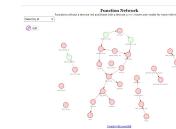
## Packaging cost-effectiveness models in R: A tutorial.

**Smith RA, Mohammed W and Schneider PP.** R Packaging cost-effectiveness models in R: A tutorial. 2023. (<https://wellcomeopenresearch.org/articles/8-419>)



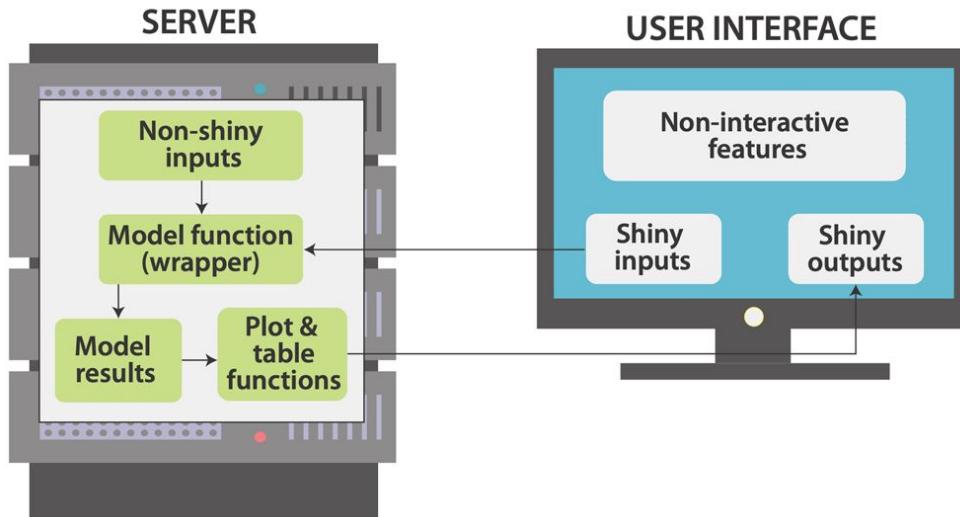
## assertHE: an R package to improve quality assurance of health economic models

**Smith et al.** assertHE: an R package to improve quality assurance of health economic models. 2024. (<https://github.com/dark-peaks-analytics/assertHE>)



# 2020 - Making Health Economic Models Shiny

## ShinyApp function



Wellcome Open Research Wellcome Open Research 2020, 5:69 Last updated: 05/03/2022

Check for updates

METHOD ARTICLE Review Making health economic models Shiny: A tutorial [version 2; peer review: 2 approved]

Robert A. Smith , Paul Schneider 

School of Health and Related Research, University of Sheffield, Regents Court, Sheffield, S1 4DA, UK

\* Equal contributors

**v2 First published:** 14 Apr 2020, 5:69  
<https://doi.org/10.12688/wellcomeopenres.15807.1>  
**Latest publication:** 31 Jul 2020, 5:69  
<https://doi.org/10.12688/wellcomeopenres.15807.2>

Open Peer Review Approval Status ✓ ✓

	1	2
version 2 (revision)	✓ 31 Jul 2020	✓ 31 Jul 2020
version 1 (revision)	?	✓ 14 Apr 2020

1. Talitha L. Feenstra, University of Groningen, Groningen, The Netherlands  
2. Yiqiao Xin , University of Glasgow, Glasgow, UK

Any reports and responses or comments on the article can be found at the end of the article.

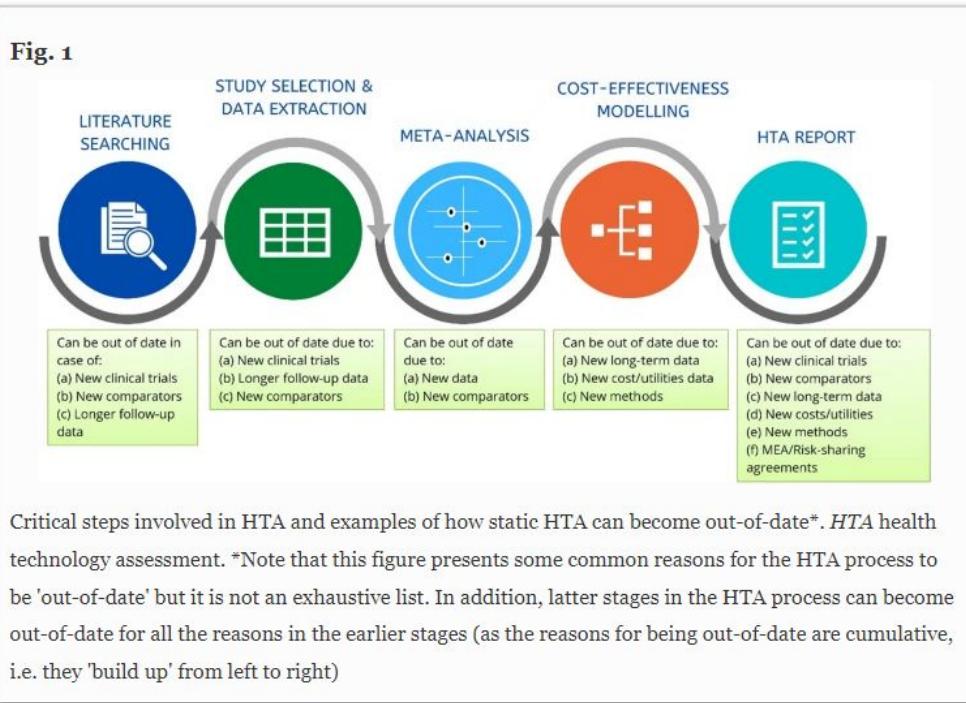
A more extensive tutorial, all code, and data are provided in a [GitHub repository](#).

**Keywords**  
Health Economics, R, RShiny, Decision Science

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# 2022 - Living HTA

**Fig. 1**



Pharmacoeconomics (2023) 41:227–237  
<https://doi.org/10.1007/s40273-022-01229-4>

LEADING ARTICLE

## Living Health Technology Assessment: Issues, Challenges and Opportunities

Praeven Thokala<sup>1</sup> · Tushar Srivastava<sup>1,2</sup> · Robert Smith<sup>1,3</sup> · Shijie Ren<sup>1</sup> · Melanie D. Whittington<sup>4</sup> · Jamie Elvidge<sup>2</sup> · Ruth Wong<sup>1</sup> · Lesley Utley<sup>1</sup>

Accepted: 4 December 2022 / Published online: 18 January 2023  
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### Abstract

Health technology assessments (HTAs) are typically performed as one-off evaluations and can potentially become out-of-date due to the availability of new data, new comparators, or other factors. Recently, living approaches have been applied to systematic reviews and network meta-analyses to enable evidence syntheses to be updated more easily. In this paper, we provide a definition of 'Living HTA' where such a living approach could be used to update HTAs over time. Living HTA could involve performing regular or scheduled updates using a traditional manual approach, or indeed in a automated manner leveraging recent technological innovations that automate parts of the HTA process. The practical implementation of living HTA using both approaches (i.e., manual approach and using semi-automation) is described along with the likely issues and challenges with planning and implementing a living HTA process. The time, resources and additional considerations outlined may prohibit living HTA from becoming the norm for every evaluation; however, scenarios where living HTA would be particularly beneficial are discussed.

### Key Points for Decision Makers

Health technology assessments (HTAs) are typically performed as one-off evaluations and can quickly become out-of-date.

Living approaches can ensure that the HTAs are up-to-date, and potentially living HTAs could be updated manually or (semi-)automatically using innovative software platforms.

However, living HTA involves substantial time, planning and resource commitments, and as such should only be used in situations where it is important to ensure the HTA is up-to-date.

### 1 Introduction

Health technology assessment (HTA) agencies perform evaluation of clinical and cost-effectiveness evidence of new interventions to decide whether they should be reimbursed.

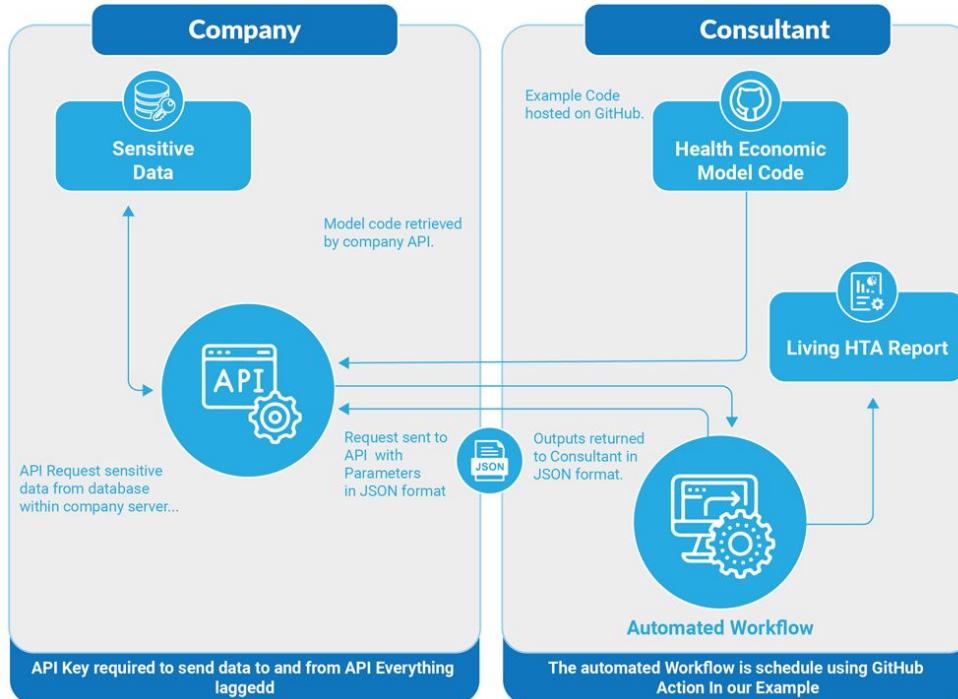
Extended author information available on the last page of the article

These are typically performed as one-off evaluations and can potentially become out-of-date due to various reasons (e.g., availability of new data, new comparators, new methods, etc.). While some HTA agencies perform updates of HTAs periodically if certain criteria are met, these updates are typically a few years apart and the details of updates may often not be communicated by the HTA agencies.

There is growing recognition of the need for the HTA process to respond to an evolving evidence base, particularly in reimbursement decisions with high uncertainty. A recent paper on living systematic reviews [1] suggests that HTAs are well placed to respond to an evolving evidence base through maturity, and proposes a model for integrating changes arising from new evidence to feed into adoption, no adoption and disinvestment decisions [1]. However, as far as we know, there is no literature on the practicalities of performing a regular update of an HTA using a living approach.

While examples of living systematic reviews and living meta-analyses are already well established, living HTA is not yet fully defined or understood. In this paper, we outline the work in progress to define what is meant by 'Living HTA' and provide a definition for living HTA and the situations in which it could be useful. While there are similarities between living HTA and the updates that HTA groups make, we outline how the living HTA process could potentially be operationalised from the current practice.

# 2022 - Living HTA



**Wellcome Open Research** Wellcome Open Research 2022, 7:194 Last updated: 24 OCT 2022

**Check for updates**

**METHOD ARTICLE**

**Living HTA: Automating Health Economic Evaluation with R [version 2; peer review: 2 approved]**

Robert A. Smith  1, Paul P. Schneider  1,3, Wael Mohammed  1,3

<sup>1</sup>School of Health and Related Research, University of Sheffield, Sheffield, S1 4DA, UK  
<sup>2</sup>Community, Sheffield, S1 2GD, UK  
<sup>3</sup>Dark Peak Analytics, Sheffield, S11 7BA, UK

**V2** First published: 21 Jul 2022, 7:194  
<https://doi.org/10.12688/wellcomeopenres.17933.1>  
Latest published: 11 Oct 2022, 7:194  
<https://doi.org/10.12688/wellcomeopenres.17933.2>

**Open Peer Review**

Approval Status	1	2
version 2		
(revision)		
11 Oct 2022		
version 1		
(revision)		
21 Jul 2022		

**Abstract**: Requiring access to sensitive data can be a significant obstacle for the development of health models in the Health Economics & Outcomes Research (HEOR) setting. We demonstrate how health economic evaluation can be conducted with minimal transfer of data between parties, while automating reporting as new information becomes available.

**Methods**: We developed an automated analysis and reporting pipeline for health economic evaluations that can be made openly available on a GitHub repository. The pipeline consists of three parts: An economic model is constructed by the consultant using pseudo data. On the data-owner side, an application programming interface (API) is hosted on a server. This API hosts all sensitive data, so that it does not need to be provided to the consultant. An automated workflow is created, which calls the API, retrieves results, and generates a report.

**Results**: The application of modern data science tools and practices allows analyses of data without the need for direct access, negating the need to share sensitive data. In addition, the entire workflow can be largely automated; the analysis can be scheduled to run at defined time points (e.g. monthly), or when triggered by an event (e.g. an update to the underlying data). The results can be generated automatically and then be reported into a report. Documents no longer need to be revised manually.

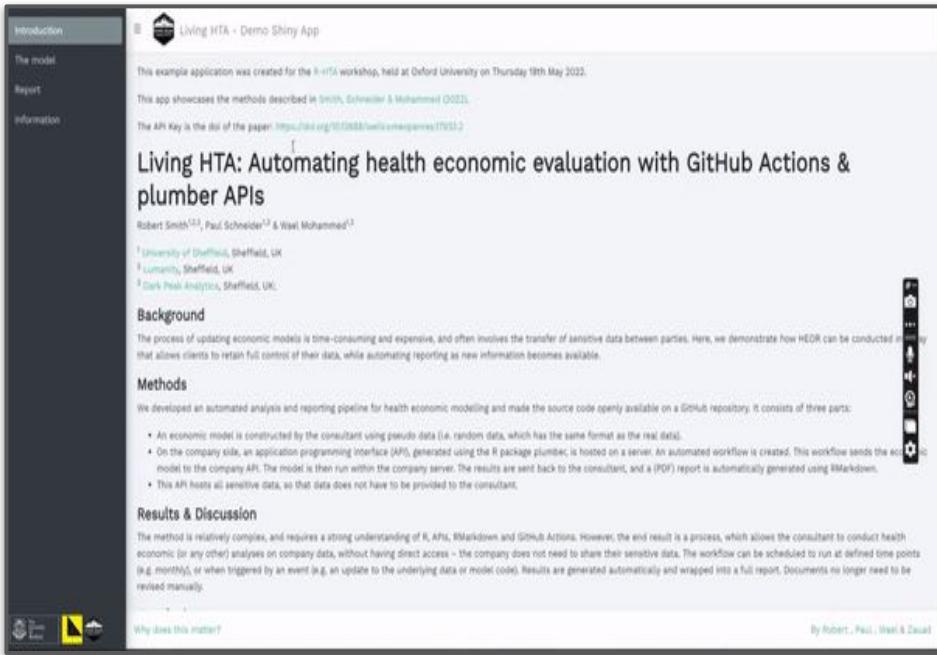
**Conclusions**: This example demonstrates that it is possible, within a HEOR setting, to separate the health economic model from the data, and automate the main steps of the analysis pipeline.

**Keywords**: HEOR, HTA, APIs, R, plumber

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**Smith RA, Schneider PP and Mohammed W.** Living HTA: Automating Health Economic Evaluation with R. *Wellcome Open Res* 2022, 7:194 (<https://doi.org/10.12688/wellcomeopenres.17933.2>)

# 2022 - Living HTA



This example application was created for the R-HTA workshop, held at Oxford University on Thursday 19th May 2022.

This app showcases the methods described in Smith, Schneider & Mohammed (2022).

The API Key is the doi of the paper: <https://doi.org/10.12688/wellcomeopenres.17933.2>

## Living HTA: Automating health economic evaluation with GitHub Actions & plumber APIs

Robert Smith<sup>1,2</sup>, Paul Schneider<sup>1,2</sup> & Wael Mohammed<sup>1,3</sup>

<sup>1</sup> University of Sheffield, Sheffield, UK  
<sup>2</sup> Luminate, Sheffield, UK  
<sup>3</sup> Dark Peak Analytics, Sheffield, UK.

### Background

The process of updating economic models is time-consuming and expensive, and often involves the transfer of sensitive data between parties. Here, we demonstrate how HEOR can be conducted in a way that allows clients to retain full control of their data, while automating reporting as new information becomes available.

### Methods

We developed an automated analysis and reporting pipeline for health economic modelling and made the source code openly available on a GitHub repository. It consists of three parts:

- An economic model is constructed by the consultant using pseudo data (i.e. random data, which has the same format as the real data).
- On the company side, an application programming interface (API), generated using the R package `plumber`, is hosted on a server. An automated workflow is created. This workflow sends the economic model to the company API. The model is then run within the company servers. The results are sent back to the consultant, and a (PDF) report is automatically generated using `Markdown`.
- This API hosts all sensitive data, so that data does not have to be provided to the consultant.

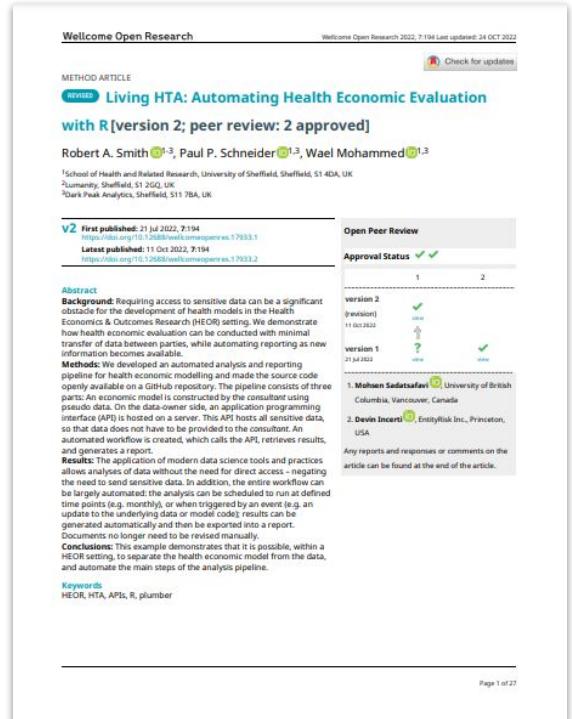
### Results & Discussion

The method is relatively complex, and requires a strong understanding of R, APIs, `Markdown` and GitHub Actions. However, the end result is a process, which allows the consultant to conduct health economic (or any other) analyses on company data, without having direct access – the company does not need to share their sensitive data. The workflow can be scheduled to run at defined time points (e.g. monthly), or when triggered by an event (e.g. an update to the underlying data or model code). Results are generated automatically and wrapped into a full report. Documents no longer need to be revised manually.

By Robert, Paul, Wael & Zauar

Why does this matter?

[https://darkpeakanalytics.shinyapps.io/living\\_HTA\\_demo/](https://darkpeakanalytics.shinyapps.io/living_HTA_demo/)



Wellcome Open Research

METHOD ARTICLE

**Living HTA: Automating Health Economic Evaluation with R [version 2; peer review: 2 approved]**

Robert A. Smith<sup>1,2</sup>, Paul P. Schneider<sup>1,2</sup>, Wael Mohammed<sup>1,3</sup>

<sup>1</sup>School of Health and Related Research, University of Sheffield, Sheffield, S1 4DA, UK  
<sup>2</sup>Luminate, Sheffield, S1 2GD, UK  
<sup>3</sup>Dark Peak Analytics, Sheffield, S11 7BA, UK

**V2** First published: 21 Jul 2022, 7:194  
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**Open Peer Review**

Approval Status	1	2
version 2	✓	
(revision)	11 Oct 2022	
version 1	?	✓
(revision)	21 Jul 2022	

1. Mahan Dastafara<sup>1</sup>, University of British Columbia, Vancouver, Canada  
2. Devin Ingersoll<sup>2</sup>, EntityRisk Inc., Princeton, USA

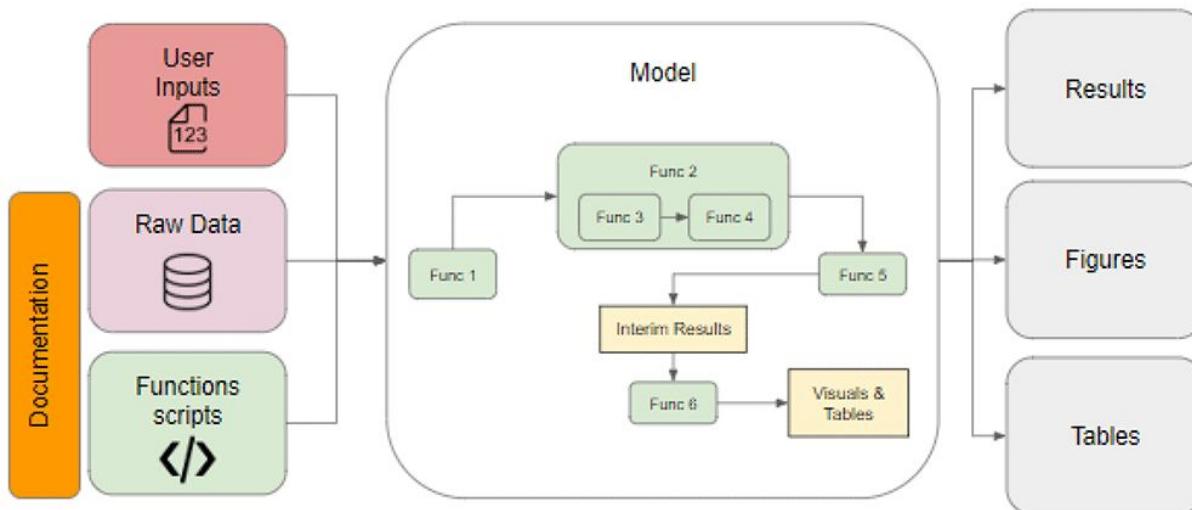
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**Smith RA, Schneider PP and Mohammed W.** Living HTA: Automating Health Economic Evaluation with R. *Wellcome Open Res* 2022, 7:194 (<https://doi.org/10.12688/wellcomeopenres.17933.2>)

# Packaging cost-effectiveness models in R: A tutorial.



Wellcome Open Research Wellcome Open Research 2023, 8:419 Last updated: 24 OCT 2023



METHOD ARTICLE

**Packaging cost-effectiveness models in R: A tutorial. [version 1; peer review: 2 approved with reservations]**

Robert Smith , Wael Mohammed , Paul Schneider 

<sup>1</sup>SchMAB, The University of Sheffield, Sheffield, England, S1 4DA, UK  
<sup>2</sup>Dark Peak Analytics, Sheffield, UK

**V1** First published: 21 Sep 2023, 8:419  
<https://doi.org/10.12688/wellcomeopenres.196561>  
Latest published: 21 Sep 2023, 8:419  
<https://doi.org/10.12688/wellcomeopenres.196561>

**Abstract**  
**Background:** The use of programming languages such as R in health economics and decision science is increasing, and brings numerous benefits including increasing model development efficiency, improving transparency, and reducing human error. However, there is limited guidance on how to best develop models using R. So far, no guidelines exist for R model development.

**Methods:** We present the advantages of creating health economic models as R packages - structured collections of functions, data sets, tests, and documentation. Assuming an intermediate understanding of R, we provide a template for creating a package to structure a R model for health economic evaluation. All source code used in or referenced by this paper is available under an open-source licence.

**Case Study:** We use the Sick Sicker Model as a case study applying the steps from the tutorial to demonstrate model development, documentation, and transparency of health economic evaluation models.

**Conclusion:** R packages offer a valuable framework for enhancing the development and transparency of health economic evaluation models. Embedded in a modern software engineering and software development practices, while fostering a collaborative culture, has the potential to significantly improve the quality of health economic models, and, ultimately, support better decision making in healthcare.

**Keywords**  
HTA, R, Open-source, Health Economics

Open Peer Review

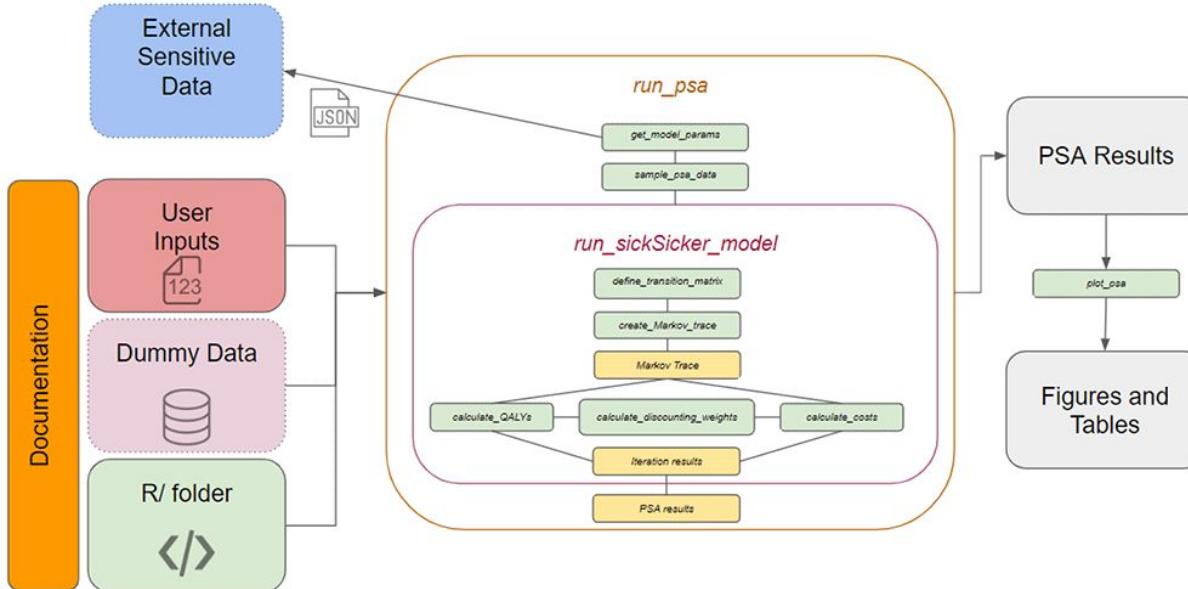
Approval Status	1	2
version 1	  	  
21 Sep 2023	  	  

1. Isaac Corra Ramos , Erasmus University Rotterdam, Rotterdam, The Netherlands  
2. Joe Mori , York Health Economics Consortium, York, UK

Any reports and responses or comments on the article can be found at the end of the article.

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# Packaging cost-effectiveness models in R: A tutorial.



Wellcome Open Research Wellcome Open Research 2023, 8:419 Last updated: 24 OCT 2023



METHOD ARTICLE

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**Abstract**  
**Background:** The use of programming languages such as R in health economics and decision science is increasing, and brings numerous benefits including increasing model development efficiency, improving transparency, and reducing human error. However, there is limited guidance on how to best develop models using R. So far, no structured framework has been proposed.

**Methods:** We present the advantages of creating health economic models as R packages - structured collections of functions, data sets, tests, and documentation. Assuming an intermediate understanding of R, we provide a template for how to structure a package for health economic evaluation. All source code used in or referenced by this paper is available under an open-source licence.

**Case Study:** We use the Sick Sicker Model as a case study applying the steps from the tutorial to demonstrate model development, testing, and peer review. This can improve the distribution of code, thereby streamlining model development, and improving methods in health economic evaluation.

**Conclusion:** R packages offer a valuable framework for enhancing the efficiency and transparency of health economic evaluation models. Embedding these models in R packages follows software development practices, while fostering a collaborative culture, has the potential to significantly improve the quality of health economic models, and, ultimately, support better decision making in healthcare.

**Keywords**  
 HTA, R, Open-source, Health Economics

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# Poll

Who is currently building health economic models in R?

Who is building models as a set of functions?

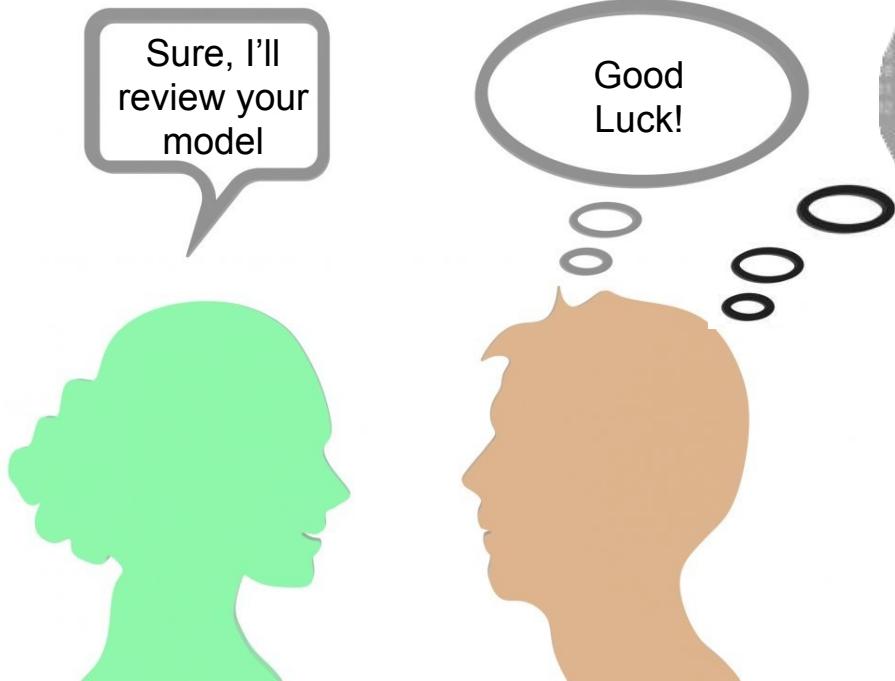
Who is building models as a package?

Who is writing unit tests for functions?

Who is assessing coverage of the unit tests?



# assertHE



```
def PRINT_HEAD
printf( " %s(%d) ", __charU__(func));
#endif
// D-Scene(C, scene) // 頂点配列清掃
(MoMvBspareG(om));
// PTMoYparePbG(MoMvBspareG(YtpareG(o)); // return;
// G=G-G=0;
(K->type == OB_ARMATURE)
{ // Y型配列 - LIB::resize(20);
bArmature *arm = (bArmature *)o->data; int i=0;
Object *o = arm->ob; Object *oM = o->id.data("OB"); C;
Object *oC = o->id.data("OB");
if(o->type == OB_ARMATURE)
{
PoseChannel *pcA = CTX_data_active_pose_bone(C), *pC=NULL, *pcB=NULL;
if(pcA&&pcA->parent&&pcA->parent->parent)
{
Object *oTarget=o->id.data("OB");
if(Vector3f(oTarget->obmat));
if((("TypeOfIK", "PoseBone", pcA)&1) return;
// M-Scene(MoMvBspareG(o));
}
```



```
58
59 population[, "AGE"] <- floor(diag_diab_population[, "CURR_AGE"])
60 population[, "MEN"] <- replace(population[, "MEN"], population[, "AGE"] > 51 & population[, "FEMALE"])
61 population[, "HBA"] <- round(diag_diab_population[, "HbA1c"], 1)
62 #This has been kept the same as in the SPHR diabetes model
63 #Record the BMI of the population
```

```
72 # calculate costs <- function(population_, parameters_, year_, alive_, GlobalVars_, treatment_, attend_se_){
```

73    #Discounted\_Costs\_per\_Patient" <- diag\_diab\_population[, "PBM"] \* population[, "BPM"] \* parameters\_[, "COST\_PBM"]

74    population\_[, "DMCOST"] [alive\_] <- population\_[, "MET"] [alive\_] \* parameters\_[, "COST\_MET"] +

75    population\_[, "MET2"] [alive\_] \* parameters\_[, "COST\_MET2"] +

76    #run population[, "INSU"] [alive\_] \* parameters\_[, "COST\_INSU"] +

77    while (year < endtime\_ &

78        sum(is.na(population[, "F\_ALLCAUSE"])) >= 1){

79        #Get all patients who are alive

80        #in population[, "atIHD\_E"] [alive\_] \* parameters\_[, "COST\_IHD\_E"] +

81        alive\_population[, "atIHD\_H"] [alive\_] \* parameters\_[, "COST\_IHD\_H"] +

82        #Create population[, "MT2\_E"] [alive\_] \* parameters\_[, "COST\_MT2\_E"] +

83        dead\_population[, "MT1\_H"] [alive\_] \* parameters\_[, "COST\_MT1\_H"] +

84        population[, "M2\_E"] [alive\_] \* (parameters\_[, "COST\_M2\_E"] +

85        #Estimate the additional costs of stroke and heart disease

86        population[, "MMI\_E"] [alive\_] \* parameters\_[, "COST\_MMIE"] +

87        #Estimate the additional costs of stroke and heart disease

88        population[, "STRO\_E"] [alive\_] \* parameters\_[, "COST\_STRO\_E"] +

89        population[, "STRO\_H"] [alive\_] \* parameters\_[, "COST\_STRO\_H"] +

90        population[, "STRO2\_E"] [alive\_] \* (parameters\_[, "COST\_STRO2\_E"] +

91        #only add on the additional costs of a 2nd stroke)

92        population[, "CHE\_E"] [alive\_] \* parameters\_[, "COST\_CHE\_E"] +

93        ## '@param random\_numbers\_ It's the array of random numbers for the number of patients'

94        ## '@return pBC is the vector of the probabilities of breast cancer

95        population[, "ATFIB\_H"] [alive\_] \* 0 + # note no cost was added

96        #Calculate the fitted value of breast cancer

97        Breast\_cancer<-function(population\_, parameters\_, year\_, alive\_){

98        #Calculate the fitted value of breast cancer

99        #FV <- parameter[, "GANC\_mu"] + they have an event & costs due to

100      parameter[, "CANB\_bta\_MEN"] \* population[, "MEN"] [alive\_] +

101      parameter[, "CANB\_bta\_BMI"] \* population[, "BMI"] [alive\_] +

102      parameter[, "CANB\_bta\_BMIMEN"] \* (population[, "MEN"] [alive\_] \* parameters\_[, "COST\_BMIMEN"] +

103      #convert to probabilities

104      pBC <- 1-exp(-exp(FV))

105      #set breast cancer risk to 0 for men

106      pBC <- ifelse(population[, "FEMALE"]==0,0,pBC)

107      #remove temporary variables generated in the function

108      rm(FV)

109      #return the probabilities

110      return(pBC)}

```
111 }
```

```
29 # calculate QALYs <- function(population_, parameters_, year_, alive_, GlobalVars_){
```

30    #calculate multiplier to adjust for a population with T2D without any

31    #COST\_M1\_E" + is a parameter determining baseline utility, set these two values to 0 for the time being

32    #COST\_M1\_H" + is a parameter determining baseline utility, set these two values to 0 for the time being

33    #Declare mean BMI, age and proportion female from Hayes et al

34    #COST\_M1\_E" + Mean\_BMI\_Hayes \* 28.4 #Mean BMI in the source of our baseline utilities

35    #COST\_M1\_H" + Mean\_Age\_Hayes \* 65.8 #Mean Age in the source of our baseline utilities

36    #COST\_STRO\_E" + Mean\_pFemale\_Hayes \* 4729/(6401+4729) #Source: Ali et al 2009

37    #Estimate the additional costs of stroke and heart disease

38    #COST\_STRO\_H" + Mean\_pFemale\_Hayes \* 4729/(6401+4781) #Source: Ali et al 2009

39    #Estimate the additional costs of stroke and heart disease

40    Util1\_b1\_mult <- parameters\_[, "UTIL\_BL"] /

41    #Util1\_b1\_mult <- parameters\_[, "UTIL\_BL"] /

42    #(0.9454933 + 0.0256466\*(1-Mean\_pFemale\_Hayes) +

43    #0.0002213\*Mean\_Age\_Hayes + 0.0000294\*(Mean\_Age\_Hayes^2))

44    #Set a random number seed for parallel processing

45    #utility prior to adjusting for BMI and events

46    #EQ5D" [alive\_] <- (0.9454933 +

47    #Set up the EQ5D scores for each individual in the group

48    #to all the individuals in the group

49    #registerDoParallel(cl = cl, .by = "BMT\_H")

50    #clusterExport(.by = "BMT\_H", cluster = cl, .value = "modelresults")

51    #modelresults <- parLapply(cl = cl,

52    #modelresults <- lapply(cl = cl, .value = "modelresults")

53    #PSAiterations,

54    #PSAiterations, .value = "modelresults")

55    #PSAiterations, .value = "modelresults")

56    #PSAiterations, .value = "modelresults")

57    #PSAiterations, .value = "modelresults")

58    #PSAiterations, .value = "modelresults")

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79    #PSAiterations, .value = "modelresults")

80    #PSAiterations, .value = "modelresults")

81    if(GlobalVars["Results\_output", "Value"] == "Summary"){

82      modelresults <- matrix(unlist(modelresults), ncol=24, byrow=T)

- GlobalVars\_ {
- build\_population.R
- Cancer\_Risks.R
- Costs.R
- Depression.R
- Generate\_Results\_Template.R
- Generate\_Results.R
- generate\_random.R
- intervention.R
- LifeTableMortality.R
- Osteoarthritis\_functions.R
- QALYs.R
- Run\_model.R
- Run\_simulation.R
- UKPDS\_82\_risk\_functions.R
- UKPDS\_90\_risk\_functions.R
- Update\_Events.R
- Update\_Pat\_Chars.R



# assertHE R package

Aim: *to help modellers build and review health economic models in R.*

Functionality:

- *Check that the objects created in models conform to standard rules (e.g. probabilities between 0 and 1).*
- *Summarise & visualise the structure of a model*
  - *Plot function network color coded by test coverage.*
  - *Click on the nodes to see function and test source code and test coverage.*
  - *Display a LLM generated summary of any function.*



# Using the assertHE R package

```
# install.packages("devtools")
devtools::install_github("dark-peak-analytics/assertHE")

library(assertHE)
```

B: insert checks for common errors into the code

```
check_trans_prob_array(a_P = a_P,
                      stop_if_not = T)
```

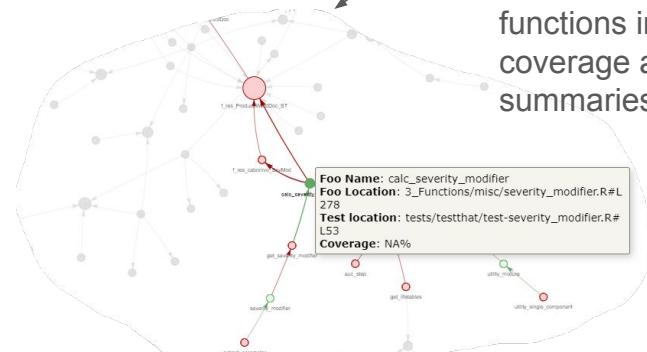
Flags if there are errors or potential problems.

```
# Warning message:
# In check_array_rows_balanced(a_P, stop_if_not = stop_if_not) :
#   Not valid transition probabilities
#   Transition probabilities not valid from Health States:
# 1 H; at cycle 1
# 2 H; at cycle 2
# 3 H; at cycle 3
# 4 H; at cycle 4
# 5 H; at cycle 5
# 6 H; at cycle 6
# 7 H; at cycle 7
# 8 H; at cycle 8
# 9 H; at cycle 9
# 10 H; at cycle 10
```

A: visualise network of functions

```
visualise_project(
  project_path = "path_to_project_directory",
  foo_path = "R",
  test_path = "tests/testthat",
  run_coverage = T)
```

Inspect the network to understand how the model functions interact, their test coverage and get AI function summaries.

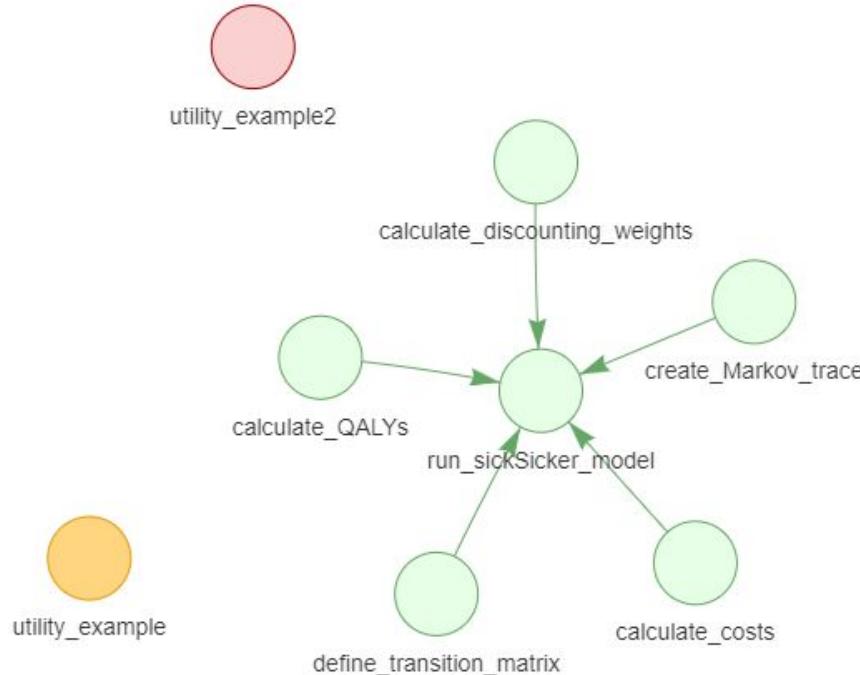


# Function Network

Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🤖 to request an AI generated summary of the corresponding function, ↗ to open the file in RStudio, or on 🌐 to load its contents into a new browser tab.



Select by id ▾



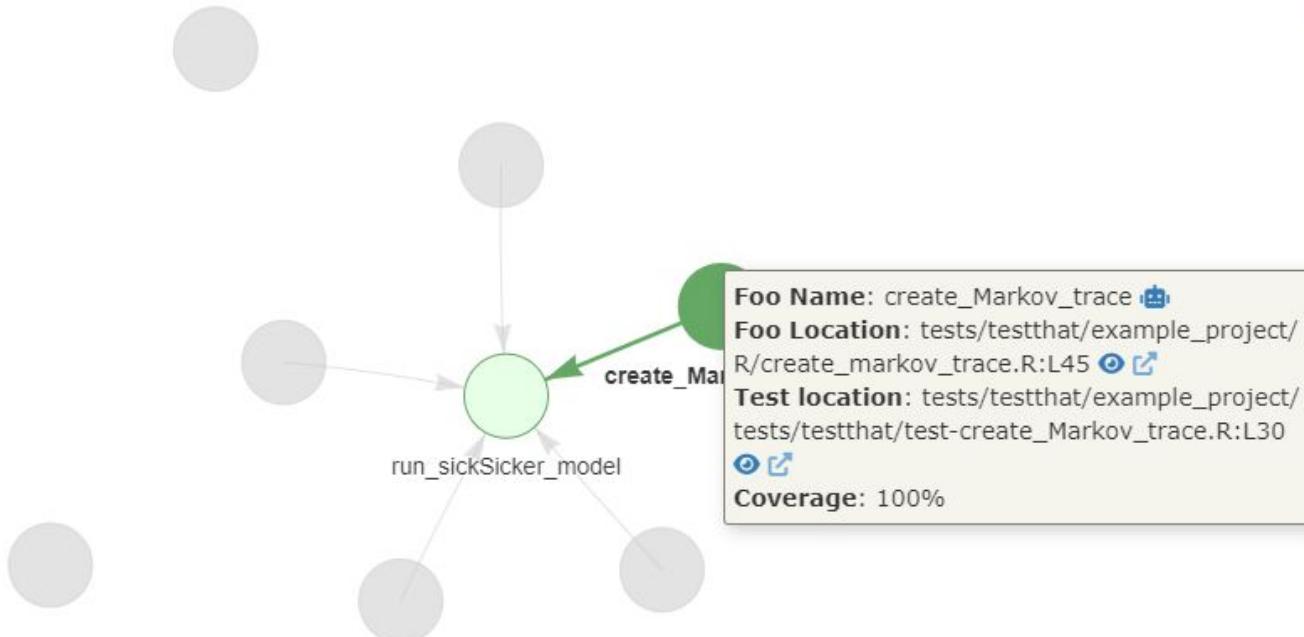
# Function Network

Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🤖 to request an AI generated summary of the corresponding function, ↗ to open the file in RStudio, or on ⓘ to load its contents into a new browser tab.



create\_Markov\_trace

ⓘ Edit



## Function Network

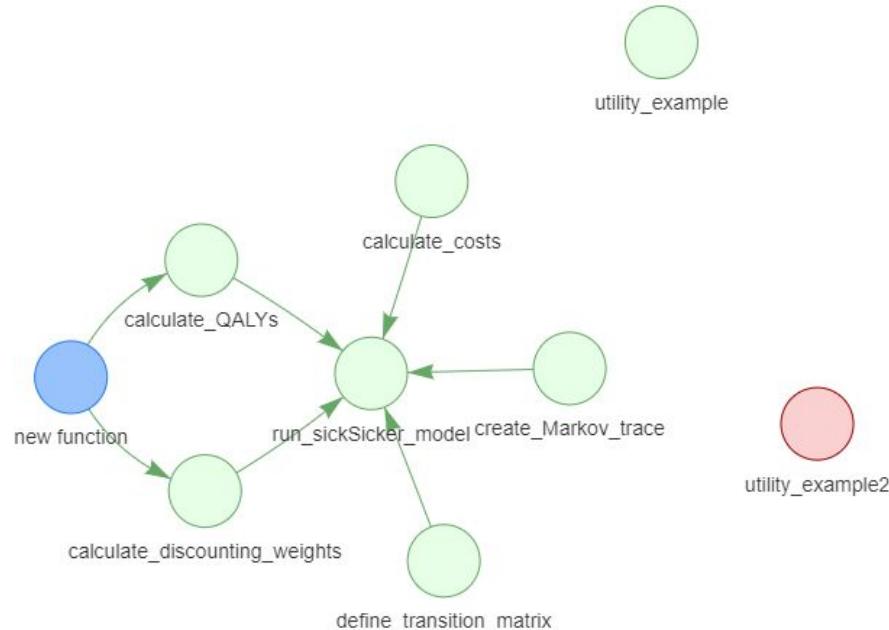
Functions without a test are **red** and those with a test are **green**. Hover over nodes for more information. Click on  to request an AI generated summary of the corresponding function,  to open the file in RStudio, or on  to load its contents into a new browser tab.

Select by id

 Add Node

 Add Edge

x



# Function Network

Functions without a test are **red** and those with a test are **green**. Hover over nodes for more information. Click on to request an AI generated summary of the corresponding function, to open the file in RStudio, or on to load its contents into a new browser tab.



create\_Markov\_trace



Edit

Click to generate LLM summary of function.

Function location

Test location

Click to view tests in tab

Click to open tests in RStudio

Testing code coverage

**Foo Name:** create\_Markov\_trace   
**Foo Location:** tests/testthat/example\_project/R/create\_markov\_trace.R:L45   
**Test location:** tests/testthat/example\_project/tests/testthat/test-create\_Markov\_trace.R:L30   
**Coverage:** 100%

Click to view function in tab

Click to open function in RStudio

# Function Network

Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🤖 to request an AI generated summary of the corresponding function, ↗ to open the file in RStudio, or on ⓘ to load its contents into a new browser tab.



create\_Markov\_trace ⓘ



Edit

Please wait ...

generating create\_Markov\_trace function summary ...

create\_Markov\_trace 🤖  
:: tests/testthat/example\_project/  
kov\_trace.R:L45 ⓘ ↗  
:: tests/testthat/example\_project/  
/test-create\_Markov\_trace.R:L30

Coverage: 100%

# Function Network

Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🤖 to request an AI generated summary of the corresponding function, ↗ to open the file in RStudio, or on ⓘ to load its contents into a new browser tab.



create\_Markov\_trace



Edit

## AI summary - create\_Markov\_trace ✕

The function 'create\_Markov\_trace' takes in a transition matrix, a time horizon, a vector of state names, and an initial trace as arguments. It first checks if the 'states\_nms\_' argument is a character vector and if the 'initial\_trace\_' argument is a numeric vector. It also verifies that the length of 'states\_nms\_' matches the length of 'initial\_trace\_' as well as the dimensions of the transition matrix.

The function then creates a Markov trace matrix with the specified time horizon and state names. It fills in the initial trace at the first row of the matrix and iteratively calculates the Markov trace at each time step by multiplying the previous trace with the transition matrix. The final output is the complete Markov trace matrix.

create\_Mat

**Foo Name:** create\_Markov\_trace 🤖

**Foo Location:** tests/testthat/example\_project/R/create\_markov\_trace.R:L45 ⓘ↗

**Test location:** tests/testthat/example\_project/tests/testthat/test-create\_Markov\_trace.R:L30 ⓘ↗

**Coverage:** 100%

# Test cases

We have used the assertHE package on several models as test cases:

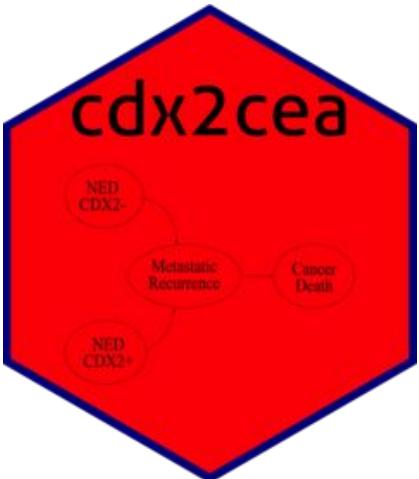
- [NICE RCC Model](#)
- [sicksickerPack](#) teaching model contained in a package.
- [cdx2cea](#) as described in [Alarid-Escudero et al. 2022](#)
- [DOACs-AF-Economic-model](#) developed by Bristol University
- The CGD AMR Cost model - in press.
- [Embedding Economics Analysis](#) Diabetes Microsimulation model described in (in press).

Please get in contact if you would like to use the package to help review a model in R.



# Case Studies

# Case Study



ScienceDirect  
Contents lists available at ScienceDirect.com  
Journal homepage: [www.elsevier.com/locate/val](http://www.elsevier.com/locate/val)

**Economic Evaluation**

**CDX2 Biomarker Testing and Adjuvant Therapy for Stage II Colon Cancer: An Exploratory Cost-Effectiveness Analysis**

Fernando Alarid-Gordales, PhD; Deborah Schrag, MD, MPH; Karen M. Kortz, ScD

**ABSTRACT**

**Objectives:** Adjuvant chemotherapy is not recommended for patients with average-risk stage II (T1N0) colon cancer, nevertheless, a subgroup of these patients who are CDX2-negative might benefit from adjuvant chemotherapy. We evaluated the cost-effectiveness of testing for the absence of CDX2 expression followed by adjuvant chemotherapy (FOLFOX) versus observation alone for patients with average-risk stage II colon cancer.

**Methods:** We developed a decision model to simulate a hypothetical cohort of 65-year-old patients with average-risk stage II colon cancer with 7.2% of these patients being CDX2-negative under 2 different interventions: (1) test for the absence of CDX2 expression followed by adjuvant chemotherapy (FOLFOX) for all patients who are CDX2-negative and observation for all patients who are CDX2-positive; (2) no chemotherapy for any patient. We derived disease progression parameters, adjuvant chemotherapy effectiveness and utilities from published analyses, and cancer care costs from the Surveillance, Epidemiology, and End Results (SEER)-Medicare database.

**Results:** Testing for CDX2 followed by FOLFOX for CDX2-negative patients had an incremental cost-effectiveness ratio of \$300,000/QALY (Quality-Adjusted Life Year) compared to observation alone. Testing for CDX2 followed by FOLFOX for CDX2-negative patients was \$100,000/QALY vs \$80,397 discounted US dollar lifetime costs. In sensitivity analysis, considering a cost-effectiveness threshold of \$100,000/QALY, testing for CDX2 followed by FOLFOX for CDX2-negative patients remains cost-effective for hazard ratios of 0.65-0.75 of the effectiveness of FOLFOX in CDX2-negative patients in reducing the rate of developing a metastatic recurrence.

**Conclusion:** Testing tumors of patients with stage II colon cancer for CDX2 and administration of adjuvant treatment to the subgroup found CDX2-negative is a cost-effective and high-value management strategy across a broad range of plausible assumptions.

**Keywords:** CDX2, cost-effectiveness analysis, decision-analytic model, immunohistochemistry testing, stage II colon cancer

**VALUE HEALTH** 2022; 25(3):409-418

---

**Introduction**

Adjuvant chemotherapy is not recommended for patients with average-risk stage II (T1N0) colon cancer,<sup>1</sup> and thus, these patients are usually treated with surgery alone. Nevertheless, a recent study by Duleba et al<sup>2</sup> described a small subgroup of patients with stage II colon cancer who were negative for the CDX2 transcription factor that associated with clinical benefit from adjuvant chemotherapy. CDX2 is a master transcription factor that has been implicated in the development of a candidate biomarker of mature colon epithelial tissues.<sup>3</sup> This study found that the absence of CDX2 expression led to a systematic search for a biomarker to identify undifferentiated tumors in a collection of human colon gene expression array experiments (National Institutes of Health Gene Expression Omnibus repository ([www.ncbi.nlm.nih.gov/geo](http://www.ncbi.nlm.nih.gov/geo))) used as a discovery data set. As a validation data set, the authors used tissue microarrays from the Cancer Diagnosis Program of the National Cancer Institute, which were analyzed for CDX2 expression by immunohistochemical (IHC) analysis. Among all tumors analyzed in the validation data set, 48 of 669 (7.2%) were CDX2-negative.<sup>2</sup> These findings were replicated in other studies showing expression in a minority of malignant epithelial cells.<sup>4,5</sup> The study also showed that CDX2-negative patients had poorer overall survival than CDX2-positive patients and CDX2-positive patients (those with biomarker expression). More importantly, the 5-year DFS was greater for the CDX2-negative patients who received adjuvant chemotherapy compared to those who did not receive adjuvant chemotherapy.

The ability to test average-risk patients with a biomarker for CDX2 has the potential to lead to larger adjuvant chemotherapy trials that may likely to be beneficial and reduce colon cancer mortality.

This study aims to quantify the long-term benefits, costs, and cost-effectiveness of testing average-risk patients with stage II colon cancer for the absence of CDX2 biomarker expression followed

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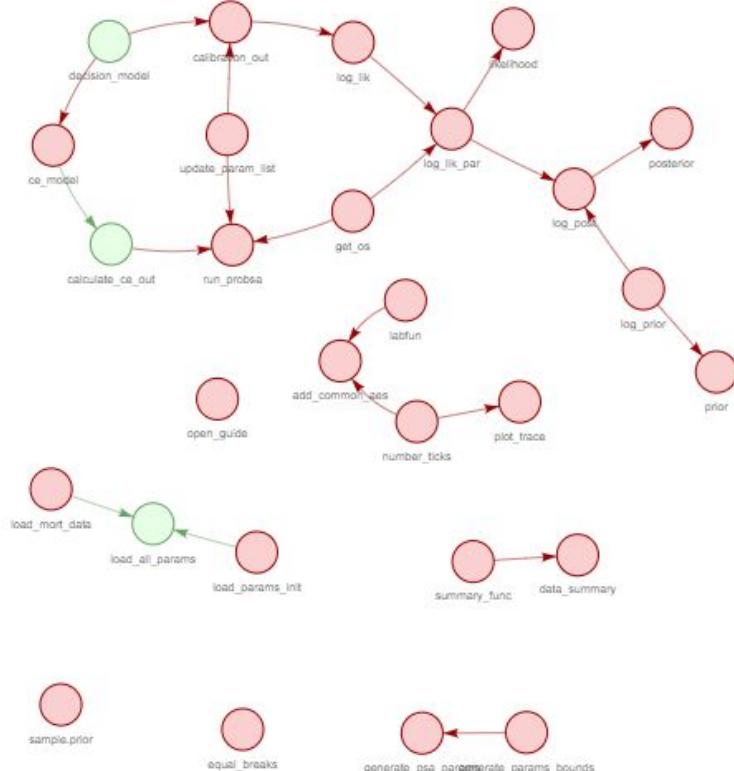
# Function Network



Functions without a test are **red** and those with a test are **green**. Hover over nodes for more information. Click on 🗺 to request an AI generated summary of the corresponding function, 📁 to open the file in RStudio, or on ⚡ to load its contents into a new browser tab.

Select by id ▾

Edit

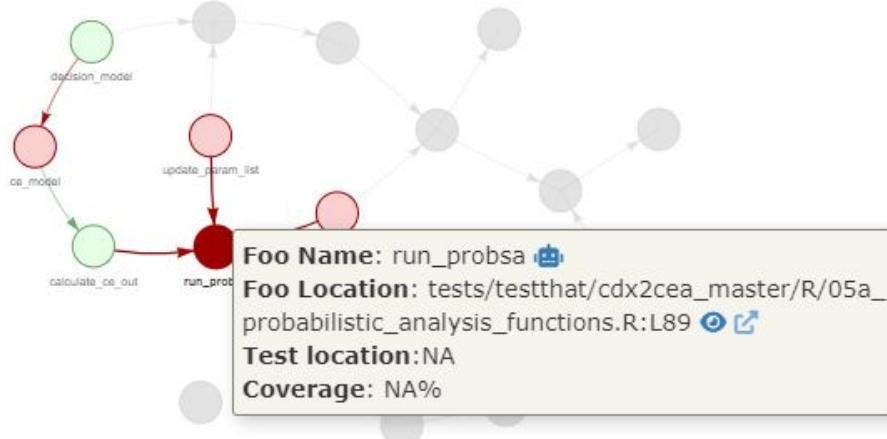


# Function Network



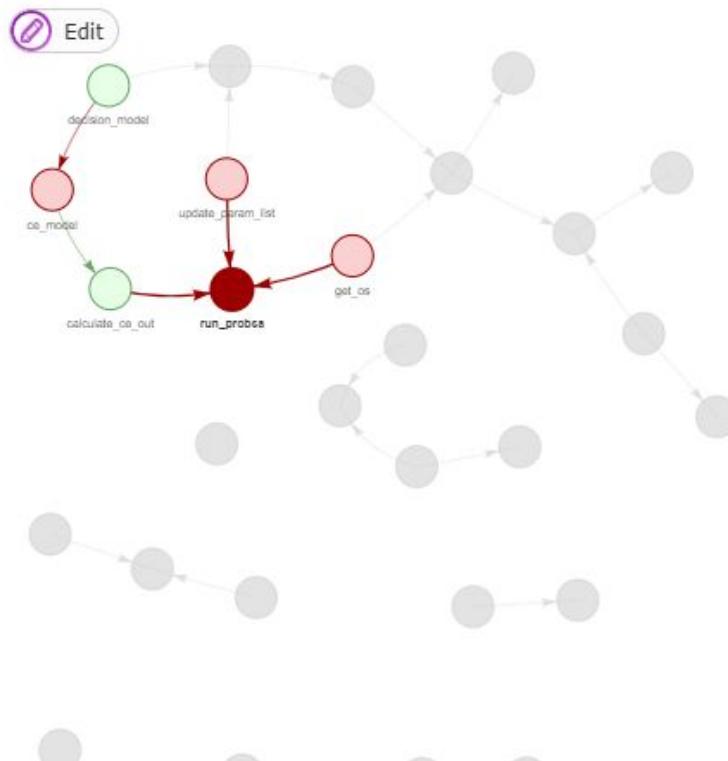
Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🤖 to request an AI generated summary of the corresponding function, ⚡ to open the file in RStudio, or on ⓘ to load its contents into a new browser tab.

run\_probsa



## Function Network

Functions without a test are **red** and those with a test are **green**. Hover over nodes for more information. Click on  to request an AI generated summary of the corresponding function,  to open the file in RStudio, or on  to load its contents into a new browser tab.

 run\_probsa
 ▼


### 05a\_probabilistic\_analysis\_functions.R

```

#'
#' \code{run_probsa} runs a probabilistic sensitivity analysis
#' calculates cost and effectiveness outcomes.
#' @param df_psa_input Data frame with ProbSA input dataset .
#' @param n_str Number of strategies
#' @param parallel Run ProbSA in parallel
#' @return
#' A list containing ProbSA cost and effectiveness outcomes f
#' @examples
#' df_psa_input <- generate_psa_params(load_all_params())
#' run_probsa(df_psa_input, parallel = FALSE)
#' @export
run_probsa <- function(df_psa_input, n_str = 2, parallel = FA
  ## Get number of simulations
  n_sim <- nrow(df_psa_input)
  if (parallel){
    ## Get OS
    os <- get_os()
    no_cores <- parallel::detectCores() - 1

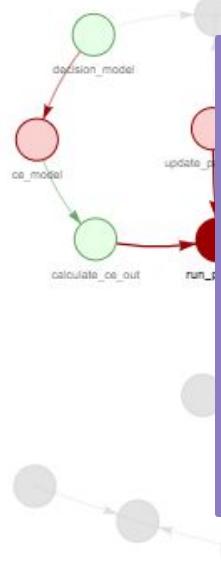
    print(paste0("Parallelized PSA on ", os, " using ", no_cc
    n_time_init_psa <- Sys.time()
  
```

# Function Network

Functions without a test are red and those with a test are green. Hover over nodes for more information. Click on 🗂️ to request an AI generated summary of the corresponding function, ↗ to open the file in RStudio, or on ⓘ to load its contents into a new browser tab.



run\_probsa



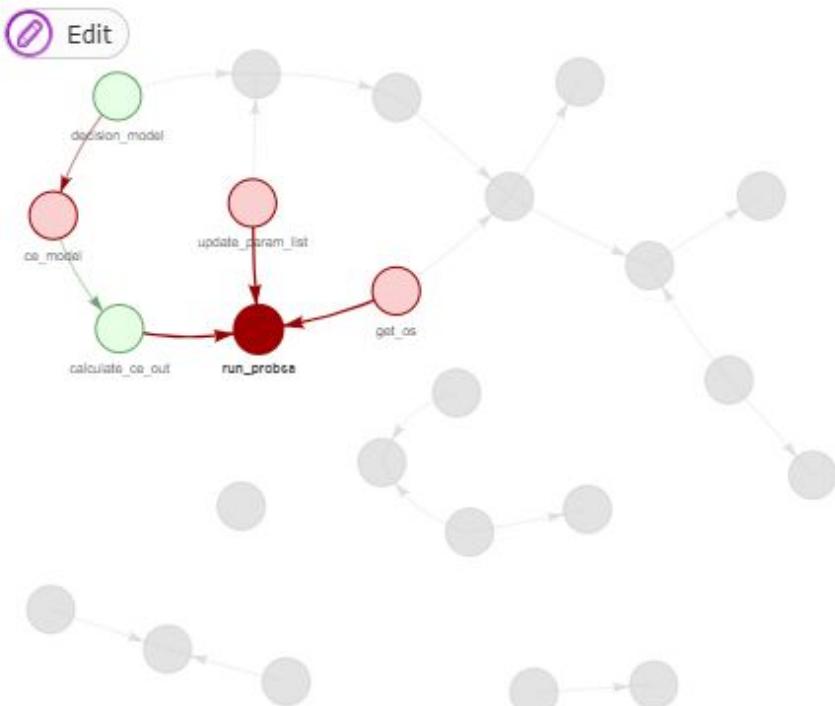
Please wait ...

generating create\_Markov\_trace function summary ...

## Function Network

Functions without a test are **red** and those with a test are **green**. Hover over nodes for more information. Click on  to request an AI generated summary of the corresponding function,  to open the file in RStudio, or on  to load its contents into a new browser tab.

run\_probsa



### AI summary - run\_probsa

...html

The 'run\_probsa' function runs probabilistic sensitivity analysis (PSA) on a given input dataset. If the 'parallel' argument is set to TRUE, the function parallelizes the PSA process using multiple cores based on the operating system. It then calculates costs and effects for each simulation, aggregates the results, and returns them in separate data frames.

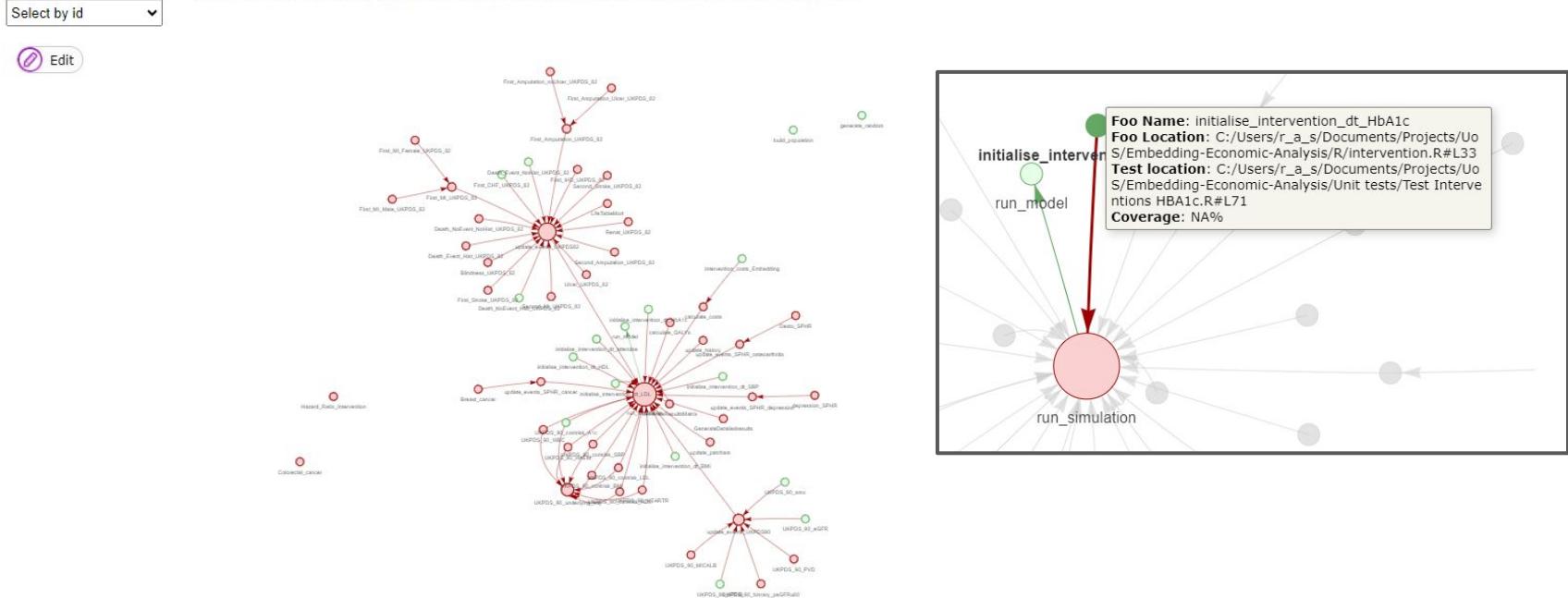
If the 'parallel' argument is set to FALSE, the function runs the PSA simulations in series. It iterates through each simulation, updates parameters, calculates costs and effects, and prints the progress. Finally, it aggregates the results and returns them in separate data frames. The function returns a list containing the costs and effects data frames.

...

# Case Study: Embedding Economic Analysis

## Embedding-Economic-Analysis Repository

Functions without a test are red and those with a test are green. Hover over nodes for more information.

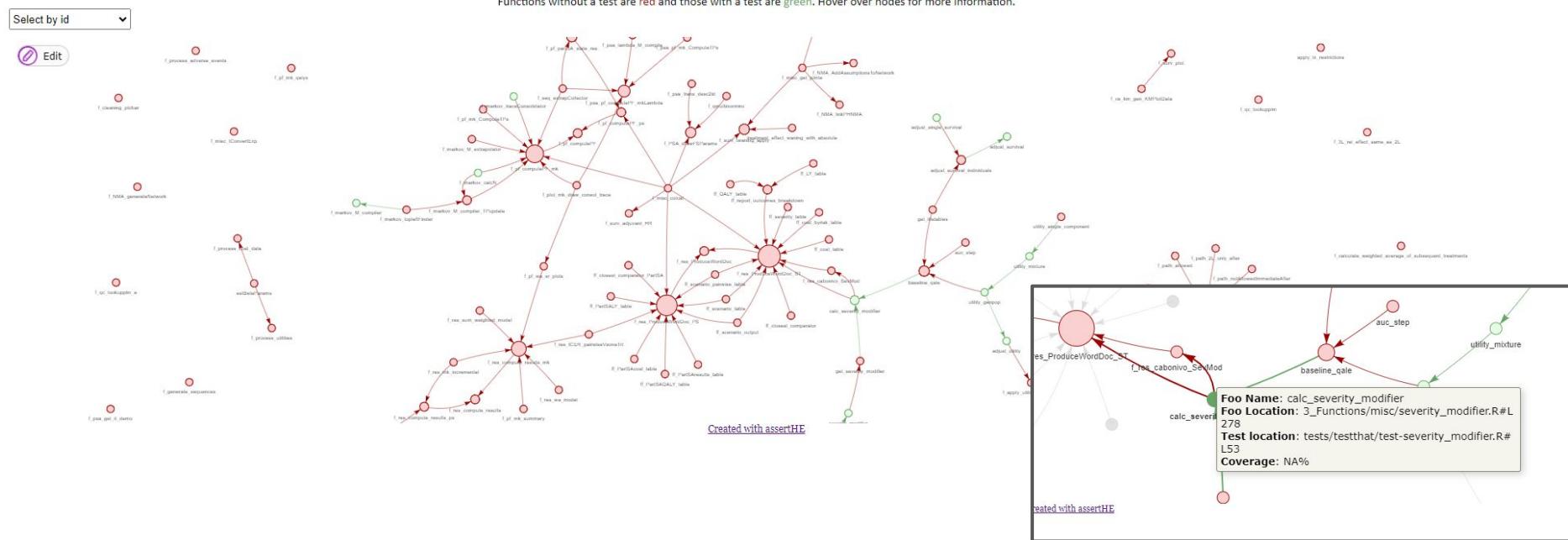


Created with assertHE

<https://github.com/DanPollardSheff/Embedding-Economic-Analysis>



# Case Study: NICE RCC Pilot



<https://vimeo.com/934769366/4895265e53?share=copy>

<https://github.com/nice-digital/NICE-model-repo>



R demo



# Next steps

# Next steps

1. Welcome contributions
  - a. Testing the software on your models
  - b. Suggesting improvements (see contribution page on GitHub)
2. Future development:
  - a. LLM Chatbot integration
  - b. Language selection
3. Open access publication + CRAN submission (Summer 24)

We would love to hear feedback on how this could be improved & potential applications.

<https://github.com/dark-peak-analytics/assertHE>

# Open Access Publication

1  
2  
3 **assertHE**: an R package to improve quality assurance of health  
4 economic models  
5  
6 Wellcome Open Research  
7

## Authors

9 Robert A Smith (Dark Peak Analytics, University of Sheffield)  
10 Yevgeniy Samyshkin (GSK),  
11 Wael Mohammed (Dark Peak Analytics, University of Sheffield)  
12 Tom Ward (GSK)  
13 Alan Martin (GSK)  
14 Sarah-Jane Anderson (GSK)  
15 Paul Schneider (Dark Peak Analytics, University of Sheffield)  
16 Baris Deniz (GSK)  
17 Dawn Lee (University of Exeter)  
18 Prof. Gianluca Baio (University College London)  
19 Howard Thom (University of Bristol)  
20 Nathan Green (University College London)  
21 Felicity Lamrock (Queens University Belfast)  
22 Brett McQueen (University of Colorado at Denver)  
23 Marina Richardson (Institute for Clinical and Economic Review)  
24 Mohamed El Alili (Zorginstituut Nederland)  
25 Xavier Pouwels (University of Twente).

March 2023

## Abstract

29

30 **Background:** Health economic evaluation models are increasingly used to inform decisions about the  
31 allocation of health care resources. Ensuring the robustness, reliability, and reproducibility of these  
32 models is critical. Currently, quality assurance is conducted by experts assessing the different  
33 components of the model manually in isolation and in combination. However, this is resource  
34 intensive. Understanding how the different components of the model fit together is time consuming,  
35 and testing each part of the model is sometimes not feasible under the timescales provided to  
36 reviewers. To aid in this, we propose the *assertHE* R package.

## Methods

37 The open source *assertHE* package provides testing functionality for modellers and reviewers of  
38 health economic models. It provides a series of common checks, which can be integrated into the  
39 model development workflow to reduce the probability of common errors. It also provides a suite of  
40 functions which allow users to better understand the network of algorithms (functions) contained in the  
41 model, where they are defined, if (and where) they are tested, and the test coverage of those that  
42 have.

43 **Results:** We applied the *assertHE* package to two health economic models, showing how to include  
44 the check functions within the model code and showing how to visualise a network of functions, see  
45 the test coverage, and obtain a Generative Pretrained Transformer (GPT) Large Language Model  
46 (LLM) generated summary of any function in the codebase. We have worked with collaborators from  
47 industry, regulators and academia to develop the package to be applicable to the widest possible  
48 range of models, making adaptations to the source code based upon feedback.

49 **Conclusions:** The *assertHE* R software package offers a toolkit for health economists building and  
50 reviewing models, facilitating a more robust and efficient quality assurance process. We hope this will  
51 ultimately improve the quality, transparency and efficiency of the health economic evaluation process  
52 for models built in R.

53

## Key Words:

54 *R, Health Economics, Unit Testing, Model Validation*

55

56

<https://github.com/dark-peak-analytics/assertHE>



# Additional resources



# R-HTA June 2024



Home Events Resources LMIC Chapter Publications Talks Tutorials People Contact



## R for trial and model-based cost-effectiveness analysis

Last updated on May 28, 2024

We are excited to announce the R for Health Technology Assessment (HTA) workshop that will be held on **Friday 28th June, Monday 1st July, and Tuesday 2nd July 2024**.

Friday 28th will be an in-person day-long, hybrid event hosted by at **ScHARR**, University of Sheffield, while the other days will be online only. Our program will be announced in May. The overall goal is to present interesting and enlightening presentations on the use of R that will engage an audience of those working in the field of health technology assessment and related analysis. Sessions may cover some or all of the following:

- New methods and applications for economic modelling using R
- Efficient modelling for economic evaluation using dedicated R packages
- Improving modelling for HTA using R – Lessons from industry and academia
- Teaching economic evaluation and HTA using R

**i** Registration for the workshop can be made at [this webpage](#). Please note that we can only accept payments via card.

The registration fee is structured as follows

Attendance type	Standard price	LMIC and students discount*
Online only (28 June, 1 and 2 July 2024)	£50	£10

13:00-14:00 Lunch

14:00-14:20 Lewis Michaelwaite Maple Health Group The design and development of the easyBIM R package

14:20-14:40 Michael O'Donnell University of Bristol REEEVR - Automated Conversion of Excel to R

14:40-15:00 Robert Smith + Tom Ward Dark Peak Analytics/University of Sheffield assertHE: an R package to improve quality assurance of health economic models

15:00-15:20 Felicity Lamrock Queen's University Belfast Closing remarks

### Day 2. Monday 1st July (Remote)

Session	Name	Institution	Title
---------	------	-------------	-------

9:00-9:10 Felicity Lamrock Queen's University Belfast Welcome

9:10-9:30 Sven Klijn Bristol Myers Squibb Modeling the Future: Pioneering the First Dossier Submission with R

9:30-9:50 Jean-Etienne Poirier Parexel Using R for Health Economics Modelling in Consulting: R (are) We There Yet?

9:50-10:10 Yi Shan Scuola IMT Alti Studi Lucca Utilizing R for Personalized Medicine: Integrating Digital Phenotyping and Health Technology Assessment

10:10-10:30 Junwen Zhou University of Oxford Estimating Costs Associated with Disease Model States Using Generalized Linear Models in R

10:30-10:45 Break

10:45-11:05 Eline Krijkamp Erasmus University Rotterdam From spreadsheet to script: Streamlining data collection and probabilistic sensitivity analysis with Excel and R

11:05-11:25 Sarwar Mozumder AstraZeneca Digitising survival curves by reconstructing individual patient-level survival data using a simulation approach

11:25-11:45 Zachary Waller Queen's University Belfast Spending time to save time: strategies for making your code run faster

11:45-12:05 Hawre Jalal University of Ottawa Introducing Grammar of Modeling R package (gmod) and the Decision Twigs graphical user interface for building HTA models

<https://r-hta.org/events/workshop/2024/>



	Topic	N	Description	*N = number of half day sessions.
<b>1</b>	Introduction to R	2	This session covers the basics of using R - this is useful to get new users up to speed prior to the rest of the course. We assume no prior knowledge of R, starting from scratch.	
<b>2</b>	Version Control with GitHub	2	Using GitHub via the RStudio GUI to manage projects, collaborate and standardise methods. This hands-on module is particularly useful for improving collaboration within organisations.	
<b>3</b>	R project workflow	1	A short module covering the basics on how to organise a project in R including R Projects, working directories, folders, data storage, effective commenting, documentation.	
<b>4</b>	Intermediate R	2	Intermediate topics in R include: iteration, writing functions, tidyverse, missing data, regression analysis, data carpentry, and code optimization.	
<b>5</b>	Partitioned Survival Models	4	Building custom PSMs in R, from survival analysis through to economic models. We assume some basic prior knowledge of survival analysis, but no knowledge of R. Optional session on the open-source 'hesim' package.	
<b>6</b>	State Transition Models	4	Building custom STMs in R with one way sensitivity analysis, probabilistic sensitivity analysis, and introduction to value of information and optimal pricing analysis. Optional session on the open-source 'heemod' package.	
<b>7</b>	Automated Reporting	4	Semi-automated (living) health economic model development using RMarkdown/Quarto and the officer package ( <a href="#">Smith et al. 2022</a> ). By the end of the course delegates will have built a semi-automated (one click update) report for a health economic model in R.	
<b>8</b>	R shiny for Health Economics	4	Building a web-based user-interface for a health economic model to allow stakeholders to run the model remotely. Largely following <a href="#">Smith &amp; Schneider (2020)</a> . By the end of the course delegates will have deployed a customised health economic model online.	
<b>9</b>	Advanced data visualisation in R	1	Using open source R packages to convey important messages using data-visualisation, including but not limited to: cost-effectiveness-planes, cost-effectiveness acceptability curves & economically justifiable pricing analysis.	
<b>10</b>	Packages for cost-effectiveness models	3	Building models in an R Package to facilitate automated documentation and testing and making it easy to standardise & share code between models. Based on a peer reviewed paper by <a href="#">Smith et al. (2023)</a> on packaging cost-effectiveness models.	
<b>11</b>	Efficient microsimulation models in R	5	This module teaches delegates to build microsimulation models in base R. It shows how to use vectorization, parallelization and C++ integration (through Rcpp) to improve the run-time of microsimulation models.	
<b>12</b>	Reviewing health economic models in R	2	This module teaches delegates how to review models built in R, including identifying common errors, black-box testing, unit testing and code coverage. It uses the assertHE R package to visualise networks of functions and insert specific checks into model code.	

[https://docs.google.com/document/d/1FpVfykhLOnvZgj1FfYcbfbpAsvqb\\_52us6xmTITLoWc/edit?usp=sharing](https://docs.google.com/document/d/1FpVfykhLOnvZgj1FfYcbfbpAsvqb_52us6xmTITLoWc/edit?usp=sharing)

# Making Health Economic Models Shiny: Sept 24



**Dr. Paul Schneider**

Paul works on conceptual and methodological problems in valuing health outcomes in economic evaluations.



**Dr. Robert Smith**

Rob works on the application of methods to improve the usability and transparency of health economic models.



**Dr. Sarah Bates**

Sarah Bates works on incorporating psychological indicators into economic models of diabetes management.

“

*Really accessible, loved the format of the website with practice questions. This made it far less daunting for a complete beginner like myself.*

Delegate from NHS Scotland

“

*The course delivery has been great! I particularly appreciate the live and updated content and the accompanying coursebook.*

Delegate from GSK

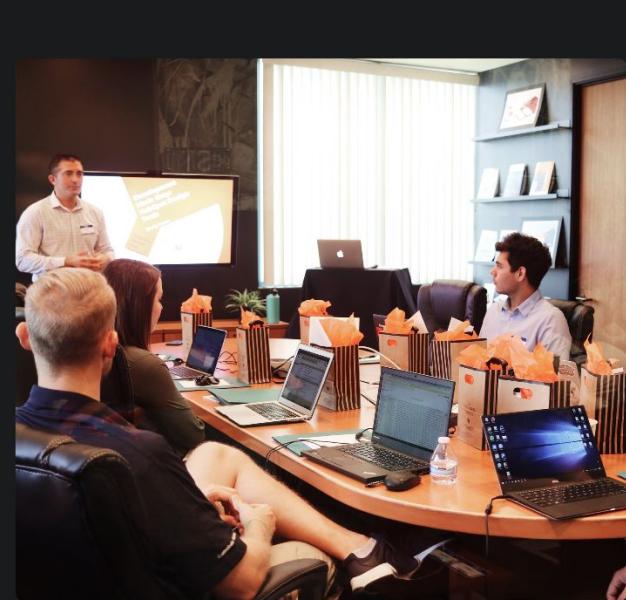
“

*It was easy to follow, every material was easily accessible and it was structured in a very manageable way.*

Delegate from UoS



# Making Health Economic Models Shiny: Sept 24



## Dates

The online course sessions are held on four consecutive Thursdays in September and October 2024:

1. Thursday, 12 September 2024
2. Thursday, 19 September 2024
3. Thursday, 26 September 2024
4. Thursday, 03 October 2024

Each session runs from:

13:00 - 16:00 GMT (London time)  
08:00 - 11:00 EST (New York time)  
17:00 - 20:00 GST (Dubai time)

**PLUS:** optional drop-in code clinics are held on Tuesdays:

1. Tuesday, 17 September 2024
2. Tuesday, 24 September 2024
3. Tuesday, 01 October 2024
4. Tuesday, 08 October 2024

Each code clinic runs from:

13:00 - 14:30 GMT (London time)  
08:00 - 09:30 EST (New York time)  
17:00 - 18:30 GST (Dubai time)

<https://www.courses.darkpeakanalytics.com/>



# Further resources

Journal Publications: [Google Scholar](#)

Open Source Code: <https://github.com/dark-peak-analytics>

Rob's talks: Talks: <https://github.com/RobertASmith/talks>

Rob's CV: [CV](#)



# assertHE: HTA R model review

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**DSMC Meeting | Robert Smith & Wael Mohammed | May 2024**

✉️ [rsmith@darkpeakanalytics.com](mailto:rsmith@darkpeakanalytics.com)

🌐 <https://github.com/dark-peak-analytics>

linkedin <https://www.linkedin.com/company/dark-peak-analytics>